

OIEP

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/027,923

DATE: 01/14/2002
TIME: 18:53:34

Input Set : A:\seqlist.txt
Output Set : N:\CRF3\01142002\J027923.raw

PS

81

3 <110> APPLICANT: Briann Gaither Bates
4 Kamalaka Gulukota
5 Yuhong Xie
6 Janet Elizabeth Paulsen
8 <120> TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
9 NUCLEIC ACID MOLECULES AND USES THEREFOR
11 <130> FILE REFERENCE: GNN-024
13 <140> CURRENT APPLICATION NUMBER: US/10/027,923
14 <141> CURRENT FILING DATE: 2001-12-21
16 <150> PRIOR APPLICATION NUMBER: 60/257,589
17 <151> PRIOR FILING DATE: 2000-12-22
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1823
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (4)..(1110)
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34 Met Val Leu Leu Leu Ile Leu Ser Val Leu Leu Leu Lys Glu Asp
35 1 5 10 15
37 gtc cgt ggg agt gca cag tcc agt gag agg agg gtg gtg gct cac atg 96
38 Val Arg Gly Ser Ala Gln Ser Ser Glu Arg Arg Val Val Ala His Met
39 20 25 30
41 ctg ggt gac atc att att gga gct ctc ttt tct gtt cat cac cag cct 144
42 Leu Gly Asp Ile Ile Ile Gly Ala Leu Phe Ser Val His His Gln Pro
43 35 40 45
45 act gtg gac gaa gtt cat gag agg aag tgt ggg gca gtc cgt gaa cag 192
46 Thr Val Asp Glu Val His Glu Arg Lys Cys Gly Ala Val Arg Glu Gln
47 50 55 60
49 tat ggc att cag aga gtg gag gcc atg ctg cat acc ctg gaa agg atc 240
50 Tyr Gly Ile Gln Arg Val Glu Ala Met Leu His Thr Leu Glu Arg Ile
51 65 70 75
53 aat tca gac ccc aca ctc ttg ccc aac atc aca ctg ggc tgt gag ata 288
54 Asn Ser Asp Pro Thr Leu Leu Pro Asn Ile Thr Leu Gly Cys Glu Ile
55 80 85 90 95
57 agg gat tcc tgc tgg cat tcg gct gtg gcc cta gag cag agc att gag 336
58 Arg Asp Ser Cys Trp His Ser Ala Val Ala Leu Glu Gln Ser Ile Glu
59 100 105 110
61 ttc ata aga gat tcc ctc att tct tcg gaa gag gaa gag ggc ttg gta 384
62 Phe Ile Arg Asp Ser Leu Ile Ser Ser Glu Glu Glu Glu Gly Leu Val
63 115 120 125
65 tgc tct gtg gat ggc tcc tcc tct tcc ttc cgc tcc aag aag ccc ata 432
66 Cys Ser Val Asp Gly Ser Ser Ser Ser Phe Arg Ser Lys Lys Pro Ile

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67          130          135          140
69 gta ggg gtc att ggg cct ggt tcc agt tct tta gcc att cag gtc cag 480
70 Val Gly Val Ile Gly Pro Gly Ser Ser Ser Leu Ala Ile Gln Val Gln
71          145          150          155
73 aat ttg ctc cag ctt ttc aac ata cct cag att gct tac tca gca acc 528
74 Asn Leu Leu Gln Leu Phe Asn Ile Pro Gln Ile Ala Tyr Ser Ala Thr
75 160          165          170          175
77 atc atg gat ctg agt gac aag act ctg ttc aaa tat ttc atg agg gtt 576
78 Ile Met Asp Leu Ser Asp Lys Thr Leu Phe Lys Tyr Phe Met Arg Val
79          180          185          190
81 gtg cct tca gat gct cag cag gca agg tcc atg gtg gac ata gtg aag 624
82 Val Pro Ser Asp Ala Gln Gln Ala Arg Ser Met Val Asp Ile Val Lys
83          195          200          205
85 agg tac aac tgg acc tat gta tca gcc gta cac aca gaa ggc aac tat 672
86 Arg Tyr Asn Trp Thr Tyr Val Ser Ala Val His Thr Glu Gly Asn Tyr
87          210          215          220
89 gga gaa agt ggg atg gaa gcc ttc aaa gat atg tca gcg aag gaa ggg 720
90 Gly Glu Ser Gly Met Glu Ala Phe Lys Asp Met Ser Ala Lys Glu Gly
91          225          230          235
93 att tgc atc gcc cac tct tac aaa atc tac agt aat gca ggg gag cag 768
94 Ile Cys Ile Ala His Ser Tyr Lys Ile Tyr Ser Asn Ala Gly Glu Gln
95 240          245          250          255
97 agc ttt gat aag ctg ctg aag aag ctc aca agt cac ttg ccc aag gcc 816
98 Ser Phe Asp Lys Leu Lys Lys Leu Thr Ser His Leu Pro Lys Ala
99          260          265          270
101 cgg gtg gtg gcc tac ttc tgt gag ggc atg acg gtg aga ggt ctg ctg 864
102 Arg Val Val Ala Tyr Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu
103          275          280          285
105 atg gcc atg agg cgc ctg ggt cta gtg gga gaa ttt ctg ctt ctg ggc 912
106 Met Ala Met Arg Arg Leu Gly Leu Val Gly Glu Phe Leu Leu Leu Gly
107          290          295          300
109 agg gaa cca gat gcc atc ttt att gag atc tca aag aac agc atc cta 960
110 Arg Glu Pro Asp Ala Ile Phe Ile Glu Ile Ser Lys Asn Ser Ile Leu
111          305          310          315
113 tgg gaa gac aga aga aaa tgc caa ggt cgc ttc ctt cag ggt ttt gga 1008
114 Trp Glu Asp Arg Arg Lys Cys Gln Gly Arg Phe Leu Gln Gly Phe Gly
115 320          325          330          335
117 gac ata tta cac aga agt gag tcc gtg ctg ctg cac atg ccc cag cct 1056
118 Asp Ile Leu His Arg Ser Glu Ser Val Leu Leu His Met Pro Gln Pro
119          340          345          350
121 ctg aat cta gag ctc agt tca ggg ccc atc act gga ctg agg gac agg 1104
122 Leu Asn Leu Glu Leu Ser Ser Gly Pro Ile Thr Gly Leu Arg Asp Arg
123          355          360          365
125 ctc atc taattctgag tggatattac tctgcattat aatgaagcca acagtcatat 1160
126 Leu Ile
128 cttctgatgt ggagatttga gaagcatttg tattggatgt gaccgtcaaa atgcgccccca 1220
130 tatcactgca acacctacaa gttttcttgc atgggggtgct cagactttca cctctggcaa 1280
132 gtattactgg gaggtccatg tggggggaactc ttggaattgg gctttcggtg tttgtaataa 1340
134 gtactggaaa gggaagaatc agaatggcaa tatatatgga gaggagggac tctttagtct 1400

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136 tgggattggtt aagaacgaca ttcagtgcag tctctttacc acctccccag ttacactgca 1460
138 gtatgtccca agacctacca accatgtagg attattcctg gattgtgaag ctagaactgt 1520
140 gagcttcggt gatgttaatc aaagctcccc tatatacacc atccctaatt gctccttctc 1580
142 acctcctctc aggcctatct tttgctgtat tcattctctga ccagagacaa atcagaaatg 1640
144 tgtttatctg ctgtgggaac ccctttatcc cataaagccc tcttccttgt gccttatcaa 1700
146 acaggacaaa taggttctgt tttatgtctt gaattgcatt ctaatgttat taaaactcat 1760
148 ttattgtgtt actattaaat gtggtaaaam cacaaaaaaa aaaaaaaaaa aaaaaaaaaa 1820
150 aaa
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 369
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 2
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160 1 5 10 15
162 Arg Gly Ser Ala Gln Ser Ser Glu Arg Arg Val Val Ala His Met Leu
163 20 25 30
165 Gly Asp Ile Ile Ile Gly Ala Leu Phe Ser Val His His Gln Pro Thr
166 35 40 45
168 Val Asp Glu Val His Glu Arg Lys Cys Gly Ala Val Arg Glu Gln Tyr
169 50 55 60
171 Gly Ile Gln Arg Val Glu Ala Met Leu His Thr Leu Glu Arg Ile Asn
172 65 70 75 80
174 Ser Asp Pro Thr Leu Leu Pro Asn Ile Thr Leu Gly Cys Glu Ile Arg
175 85 90 95
177 Asp Ser Cys Trp His Ser Ala Val Ala Leu Glu Gln Ser Ile Glu Phe
178 100 105 110
180 Ile Arg Asp Ser Leu Ile Ser Ser Glu Glu Glu Glu Gly Leu Val Cys
181 115 120 125
183 Ser Val Asp Gly Ser Ser Ser Ser Phe Arg Ser Lys Lys Pro Ile Val
184 130 135 140
186 Gly Val Ile Gly Pro Gly Ser Ser Ser Leu Ala Ile Gln Val Gln Asn
187 145 150 155 160
189 Leu Leu Gln Leu Phe Asn Ile Pro Gln Ile Ala Tyr Ser Ala Thr Ile
190 165 170 175
192 Met Asp Leu Ser Asp Lys Thr Leu Phe Lys Tyr Phe Met Arg Val Val
193 180 185 190
195 Pro Ser Asp Ala Gln Gln Ala Arg Ser Met Val Asp Ile Val Lys Arg
196 195 200 205
198 Tyr Asn Trp Thr Tyr Val Ser Ala Val His Thr Glu Gly Asn Tyr Gly
199 210 215 220
201 Glu Ser Gly Met Glu Ala Phe Lys Asp Met Ser Ala Lys Glu Gly Ile
202 225 230 235 240
204 Cys Ile Ala His Ser Tyr Lys Ile Tyr Ser Asn Ala Gly Glu Gln Ser
205 245 250 255
207 Phe Asp Lys Leu Leu Lys Lys Leu Thr Ser His Leu Pro Lys Ala Arg
208 260 265 270
210 Val Val Ala Tyr Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu Met
211 275 280 285

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213 Ala Met Arg Arg Leu Gly Leu Val Gly Glu Phe Leu Leu Leu Gly Arg
214      290      295      300
216 Glu Pro Asp Ala Ile Phe Ile Glu Ile Ser Lys Asn Ser Ile Leu Trp
217 305      310      315      320
219 Glu Asp Arg Arg Lys Cys Gln Gly Arg Phe Leu Gln Gly Phe Gly Asp
220      325      330      335
222 Ile Leu His Arg Ser Glu Ser Val Leu Leu His Met Pro Gln Pro Leu
223      340      345      350
225 Asn Leu Glu Leu Ser Ser Gly Pro Ile Thr Gly Leu Arg Asp Arg Leu
226      355      360      365
228 Ile
232 <210> SEQ ID NO: 3
233 <211> LENGTH: 1110
234 <212> TYPE: DNA
235 <213> ORGANISM: Homo sapiens
237 <220> FEATURE:
238 <221> NAME/KEY: CDS
239 <222> LOCATION: (1)..(1110)
241 <400> SEQUENCE: 3
242 atg gtc ctt ctg ttg atc ctg tca gtc tta ctt ttg aaa gaa gat gtc 48
243 Met Val Leu Leu Leu Ile Leu Ser Val Leu Leu Leu Lys Glu Asp Val
244 1      5      10      15
246 cgt ggg agt gca cag tcc agt gag agg agg gtg gtg gct cac atg ctg 96
247 Arg Gly Ser Ala Gln Ser Ser Glu Arg Arg Val Val Ala His Met Leu
248      20      25      30
250 ggt gac atc att att gga gct ctc ttt tct gtt cat cac cag cct act 144
251 Gly Asp Ile Ile Ile Gly Ala Leu Phe Ser Val His His Gln Pro Thr
252      35      40      45
254 gtg gac gaa gtt cat gag agg aag tgt ggg gca gtc cgt gaa cag tat 192
255 Val Asp Glu Val His Glu Arg Lys Cys Gly Ala Val Arg Glu Gln Tyr
256      50      55      60
258 ggc att cag aga gtg gag gcc atg ctg cat acc ctg gaa agg atc aat 240
259 Gly Ile Gln Arg Val Glu Ala Met Leu His Thr Leu Glu Arg Ile Asn
260 65      70      75      80
262 tca gac ccc aca ctc ttg ccc aac atc aca ctg ggc tgt gag ata agg 288
263 Ser Asp Pro Thr Leu Leu Pro Asn Ile Thr Leu Gly Cys Glu Ile Arg
264      85      90      95
266 gat tcc tgc tgg cat tcg gct gtg gcc cta gag cag agc att gag ttc 336
267 Asp Ser Cys Trp His Ser Ala Val Ala Leu Glu Gln Ser Ile Glu Phe
268      100      105      110
270 ata aga gat tcc ctc att tct tcg gaa gag gaa gag ggc ttg gta tgc 384
271 Ile Arg Asp Ser Leu Ile Ser Ser Glu Glu Glu Glu Gly Leu Val Cys
272      115      120      125
274 tct gtg gat ggc tcc tcc tct tcc ttc cgc tcc aag aag ccc ata gta 432
275 Ser Val Asp Gly Ser Ser Ser Ser Phe Arg Ser Lys Lys Pro Ile Val
276      130      135      140
278 ggg gtc att ggg cct ggt tcc agt tct tta gcc att cag gtc cag aat 480
279 Gly Val Ile Gly Pro Gly Ser Ser Ser Leu Ala Ile Gln Val Gln Asn
280 145      150      155      160

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282 ttg ctc cag ctt ttc aac ata cct cag att gct tac tca gca acc atc 528
283 Leu Leu Gln Leu Phe Asn Ile Pro Gln Ile Ala Tyr Ser Ala Thr Ile
284 165 170 175
286 atg gat ctg agt gac aag act ctg ttc aaa tat ttc atg agg gtt gtg 576
287 Met Asp Leu Ser Asp Lys Thr Leu Phe Lys Tyr Phe Met Arg Val Val
288 180 185 190
290 cct tca gat gct cag cag gca agg tcc atg gtg gac ata gtg aag agg 624
291 Pro Ser Asp Ala Gln Gln Ala Arg Ser Met Val Asp Ile Val Lys Arg
292 195 200 205
294 tac aac tgg acc tat gta tca gcc gta cac aca gaa ggc aac tat gga 672
295 Tyr Asn Trp Thr Tyr Val Ser Ala Val His Thr Glu Gly Asn Tyr Gly
296 210 215 220
298 gaa agt ggg atg gaa gcc ttc aaa gat atg tca gcg aag gaa ggg att 720
299 Glu Ser Gly Met Glu Ala Phe Lys Asp Met Ser Ala Lys Glu Gly Ile
300 225 230 235 240
302 tgc atc gcc cac tct tac aaa atc tac agt aat gca ggg gag cag agc 768
303 Cys Ile Ala His Ser Tyr Lys Ile Tyr Ser Asn Ala Gly Glu Gln Ser
304 245 250 255
306 ttt gat aag ctg ctg aag aag ctc aca agt cac ttg ccc aag gcc cgg 816
307 Phe Asp Lys Leu Leu Lys Lys Leu Thr Ser His Leu Pro Lys Ala Arg
308 260 265 270
310 gtg gtg gcc tac ttc tgt gag ggc atg acg gtg aga ggt ctg ctg atg 864
311 Val Val Ala Tyr Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu Met
312 275 280 285
314 gcc atg agg cgc ctg ggt cta gtg gga gaa ttt ctg ctt ctg ggc agg 912
315 Ala Met Arg Arg Leu Gly Leu Val Gly Glu Phe Leu Leu Leu Gly Arg
316 290 295 300
318 gaa cca gat gcc atc ttt att gag atc tca aag aac agc atc cta tgg 960
319 Glu Pro Asp Ala Ile Phe Ile Glu Ile Ser Lys Asn Ser Ile Leu Trp
320 305 310 315 320
322 gaa gac aga aga aaa tgc caa ggt cgc ttc ctt cag ggt ttt gga gac 1008
323 Glu Asp Arg Arg Lys Cys Gln Gly Arg Phe Leu Gln Gly Phe Gly Asp
324 325 330 335
326 ata tta cac aga agt gag tcc gtg ctg ctg cac atg ccc cag cct ctg 1056
327 Ile Leu His Arg Ser Glu Ser Val Leu Leu His Met Pro Gln Pro Leu
328 340 345 350
330 aat cta gag ctc agt tca ggg ccc atc act gga ctg agg gac agg ctc 1104
331 Asn Leu Glu Leu Ser Ser Gly Pro Ile Thr Gly Leu Arg Asp Arg Leu
332 355 360 365
334 atc taa 1110
335 Ile

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339 <210> SEQ ID NO: 4
340 <211> LENGTH: 1212
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 4
345 Met Val Leu Leu Leu Ile Leu Ser Val Leu Leu Leu Lys Glu Asp Val
346 1 5 10 15

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PSI Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

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L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6